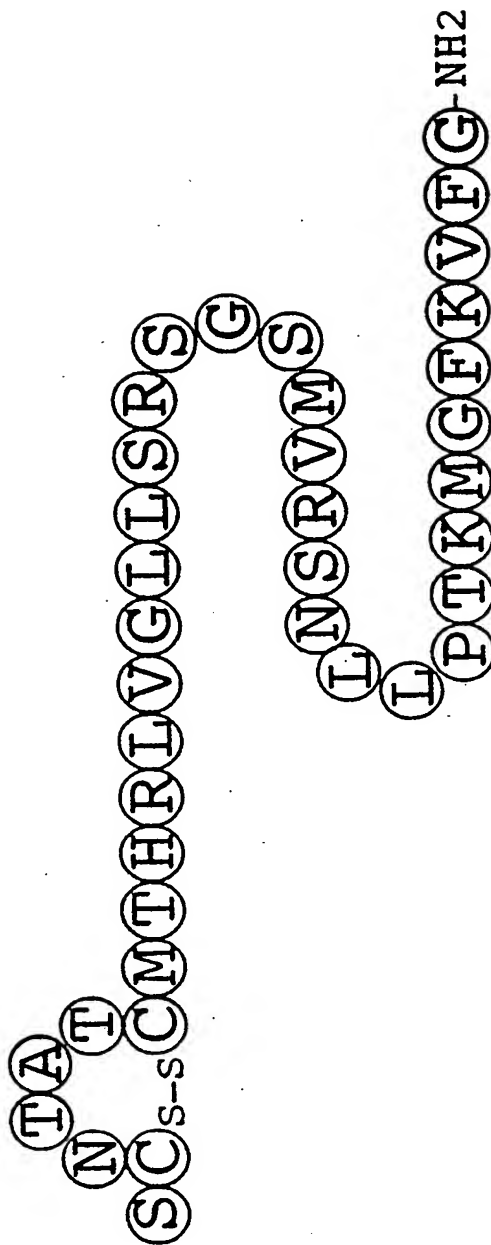




Fig. 1



PCRSP
PCGRP-I
HCGRP-I
HCGRP-II
hAmylin
pCT
hAM

SCNTATCMTHRLVGLLSRSGSMVRSNLLPTKMGEKVF_g-NH₂
SCNTATCVTHRLAGLLSRSGGMVKS_gNFVPTDVGSEAF-NH₂
ACDTATCVTHRLAGLLSRSGGVVKNNFVPTNVGSKAF-NH₂
ACNTATCVTHRLAGLLSRSGGMVKS_gNFVPTNVGSKAF-NH₂
KCNTATCATQRLANFLVHSSNNFGAILSSSTNVGSNTY-NH₂
CSNLSTCVLSAYWRNLNNFHRFSGMGFGPETP-NH₂

YRQSMN_gNFQGLRSFGCRFGTCTVQKLAHQIYQFTDKDKDNVAPRSKIS_gPQGY-NH₂

Fig. 2

Fig. 3

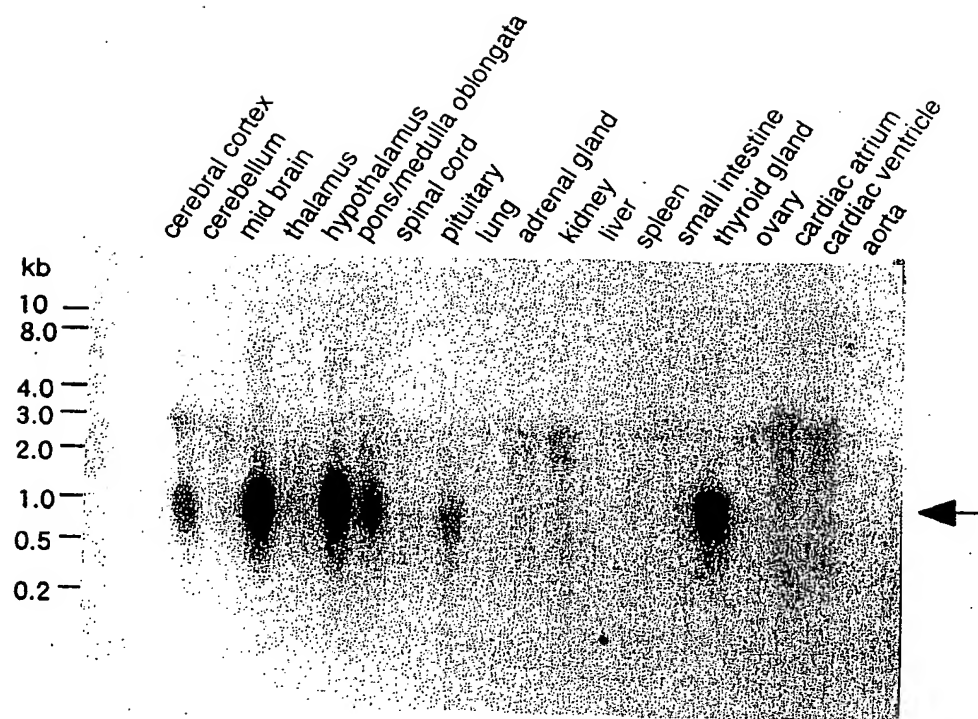


Fig. 4

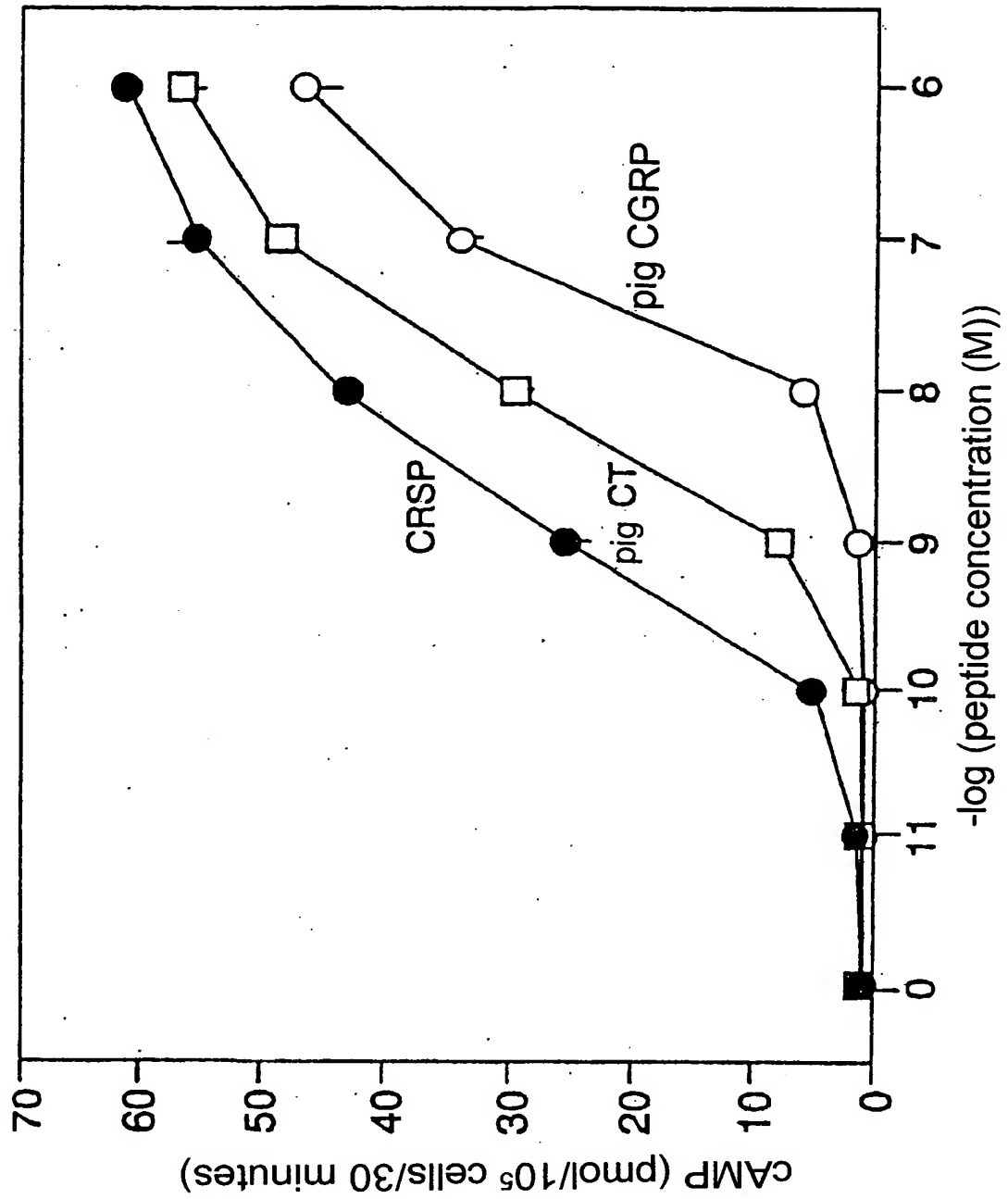


Fig. 5

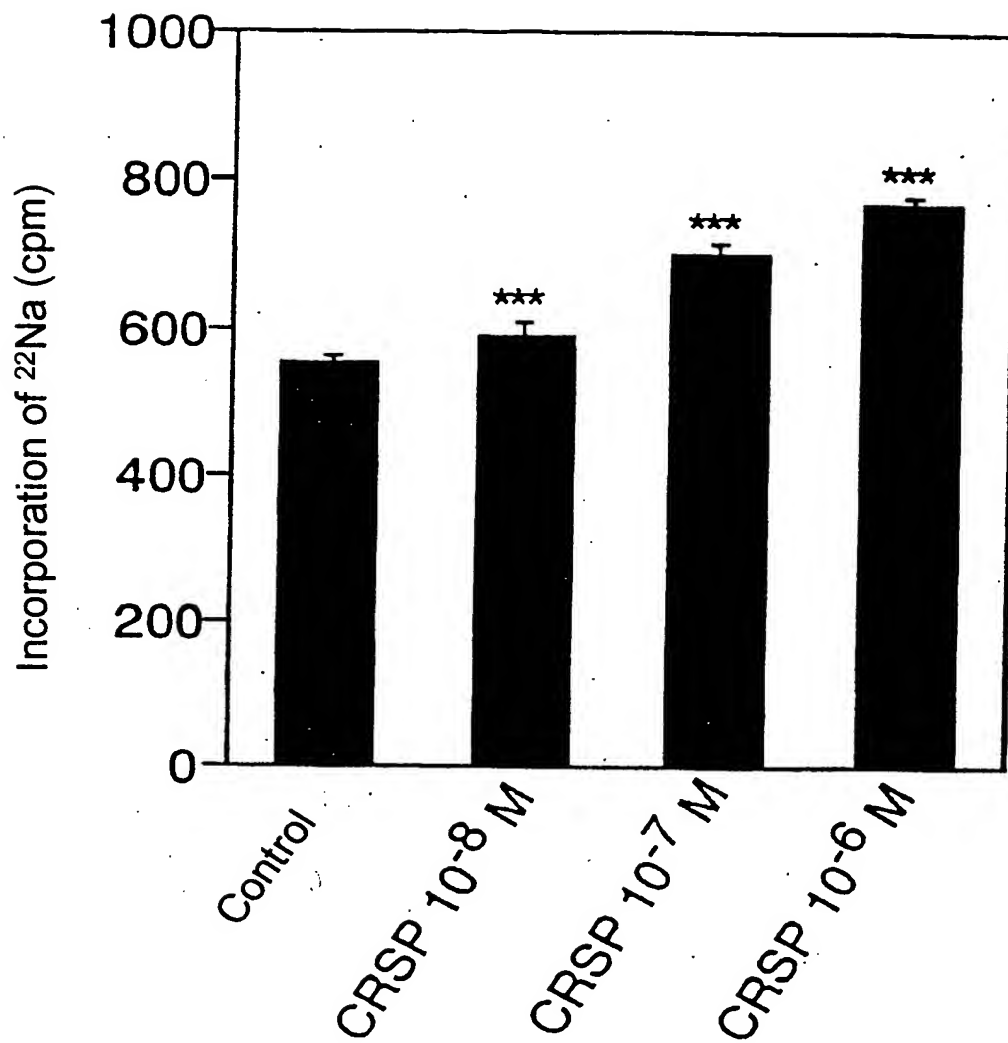


Fig. 6

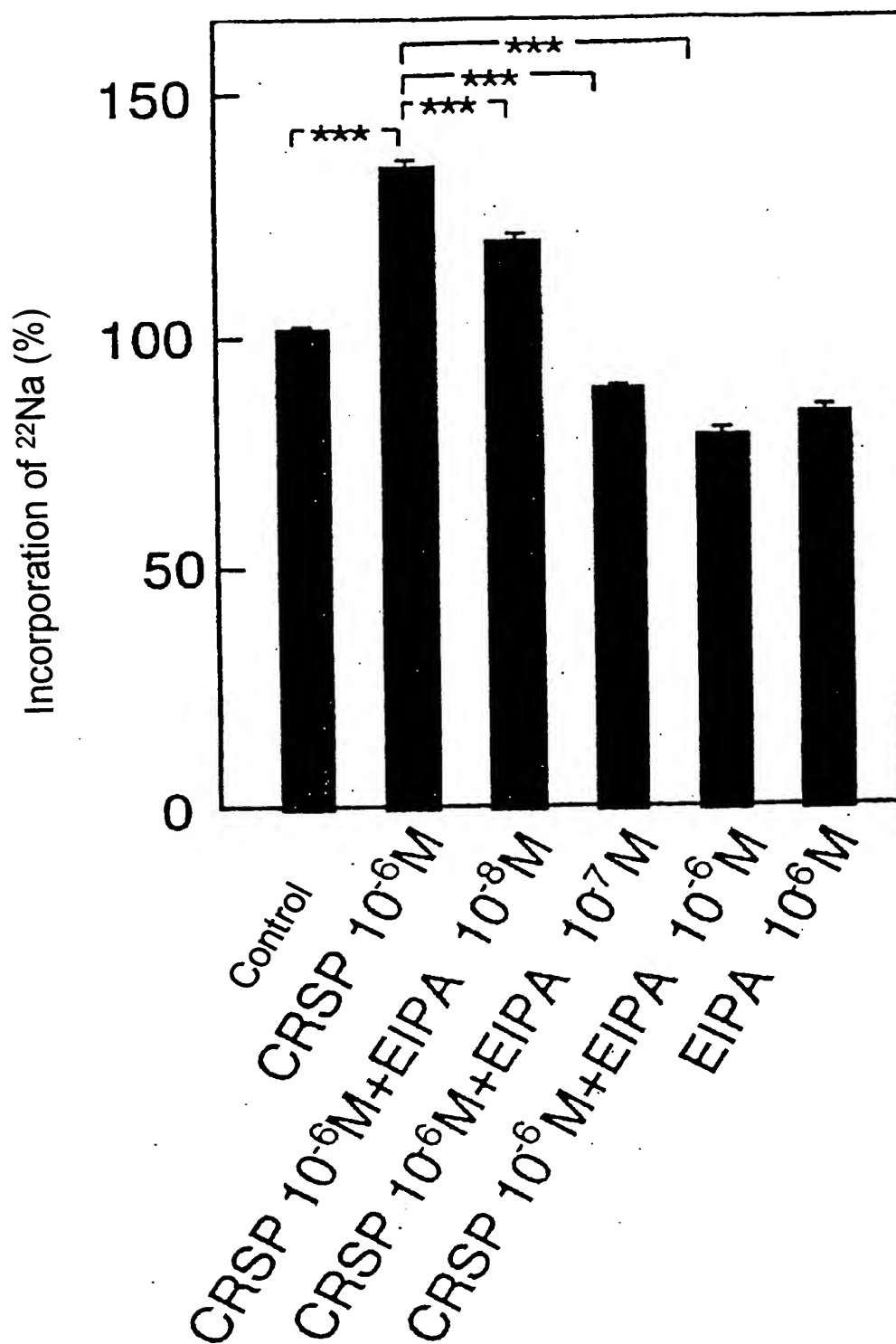


Fig. 7

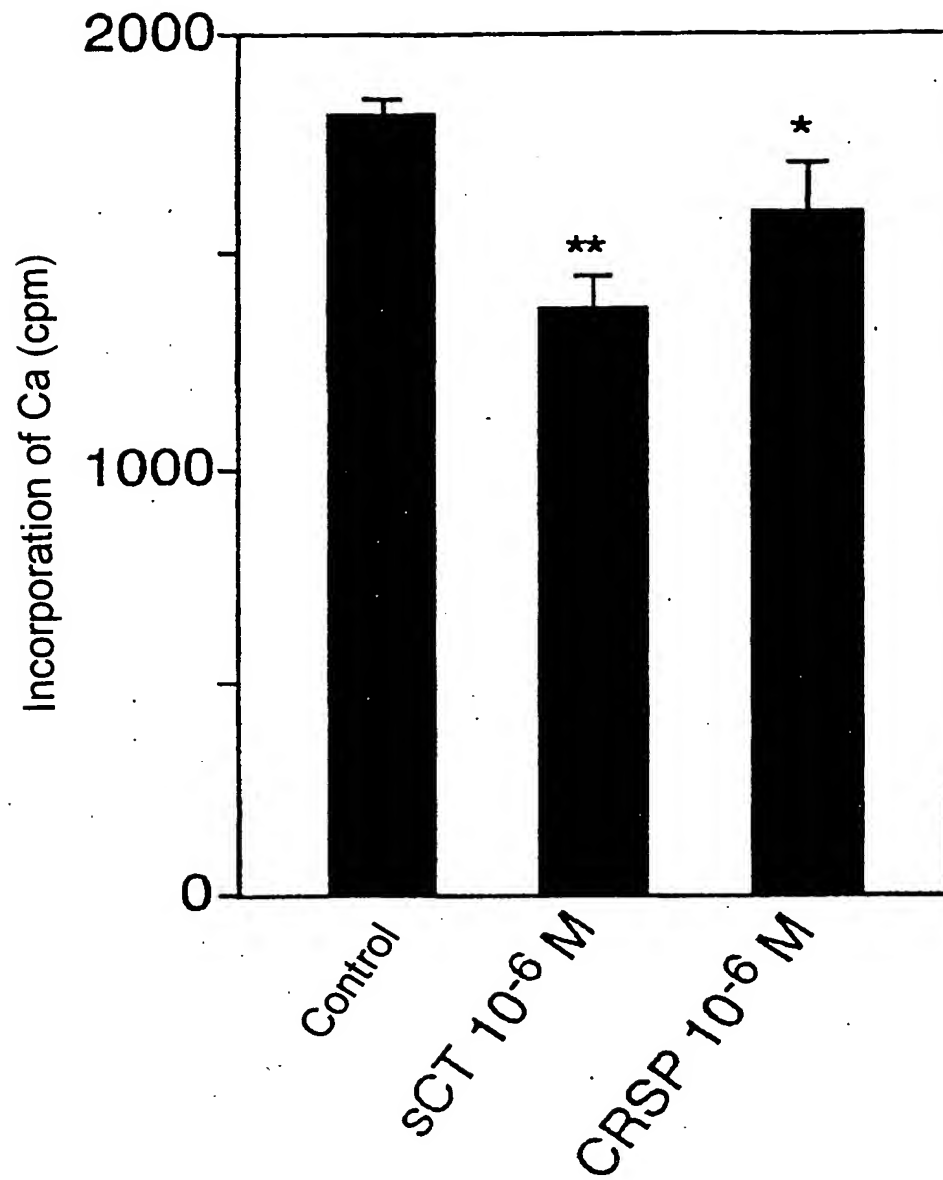


Fig. 8

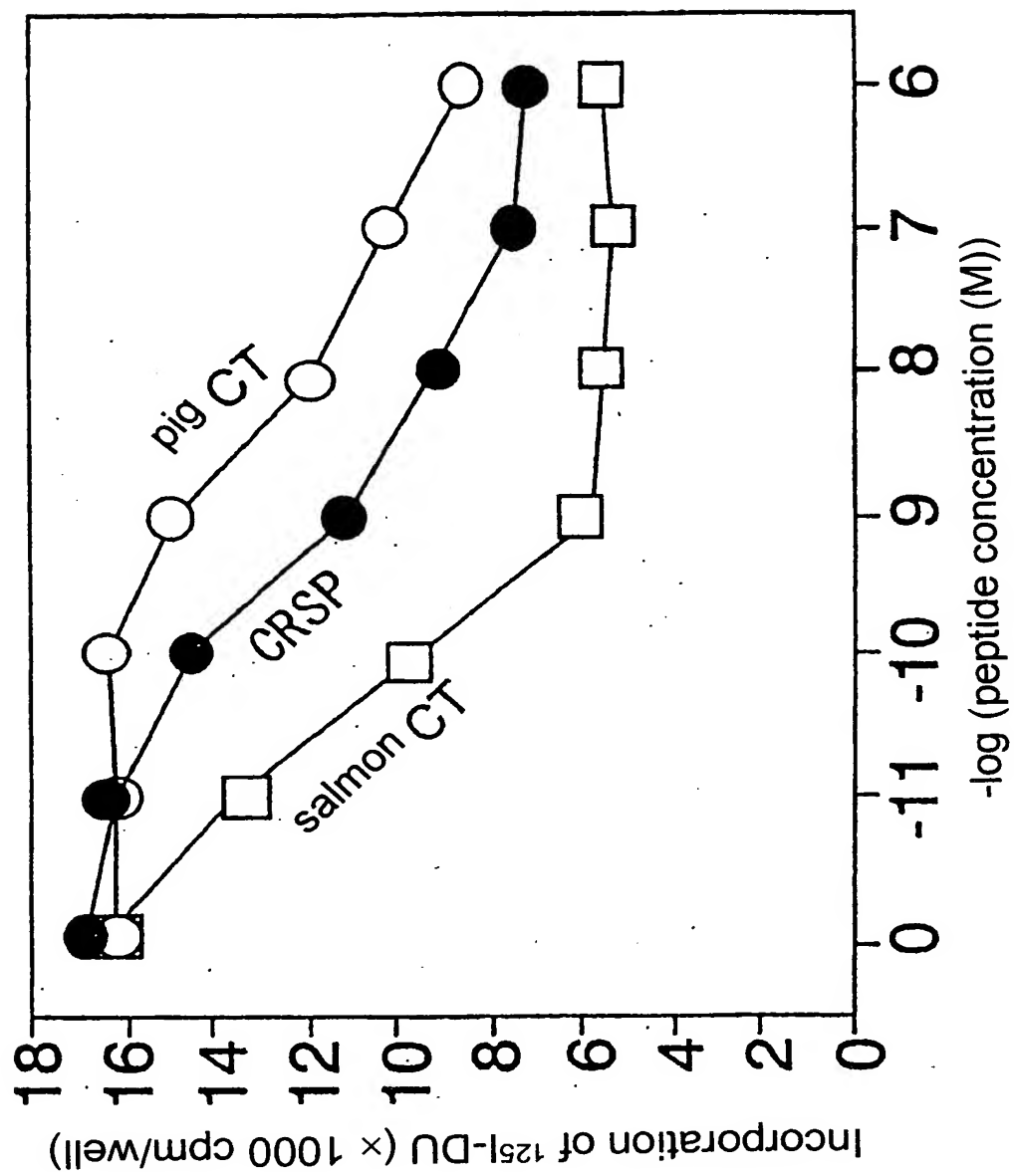


Fig. 9

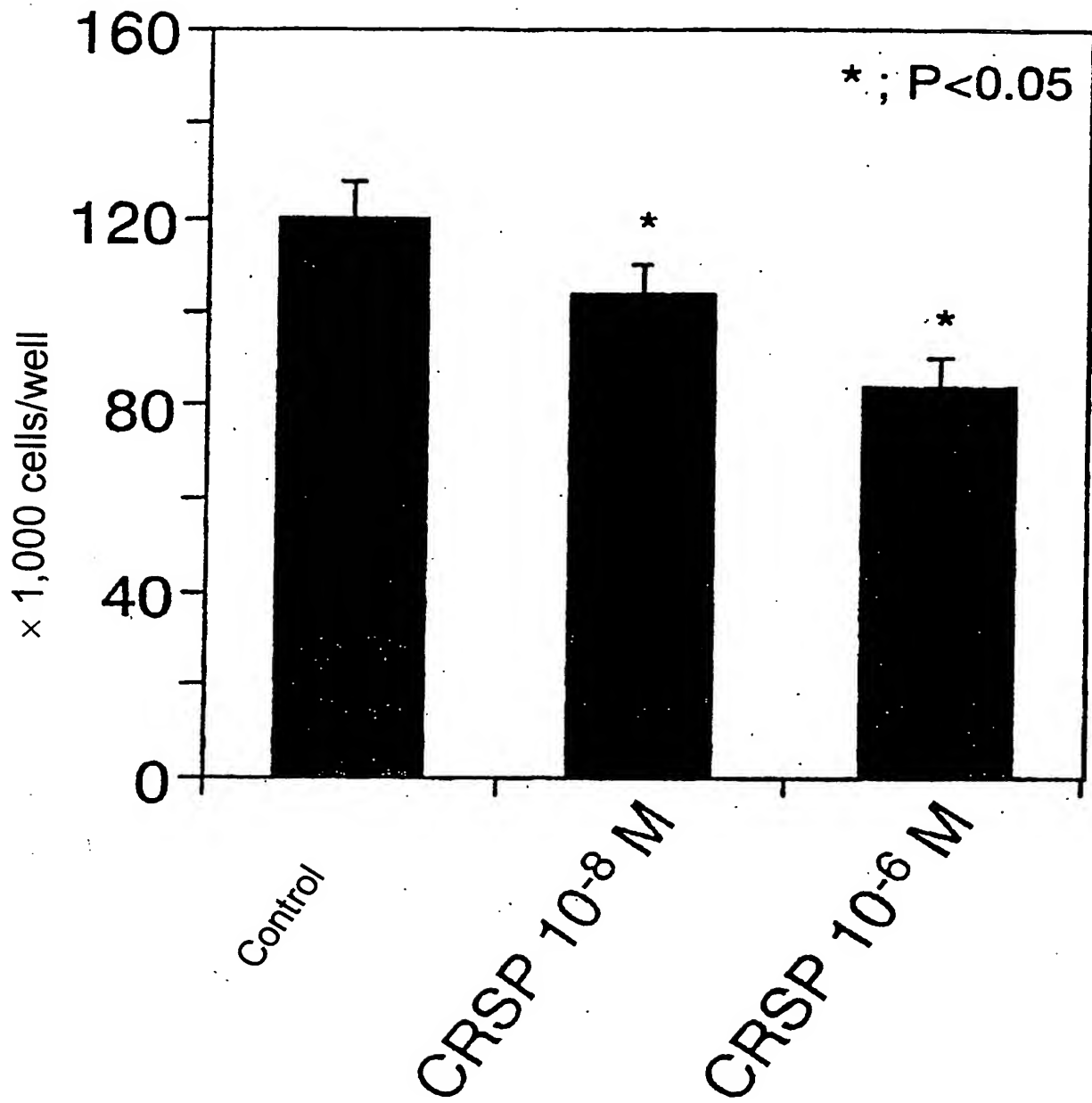


Fig. 10

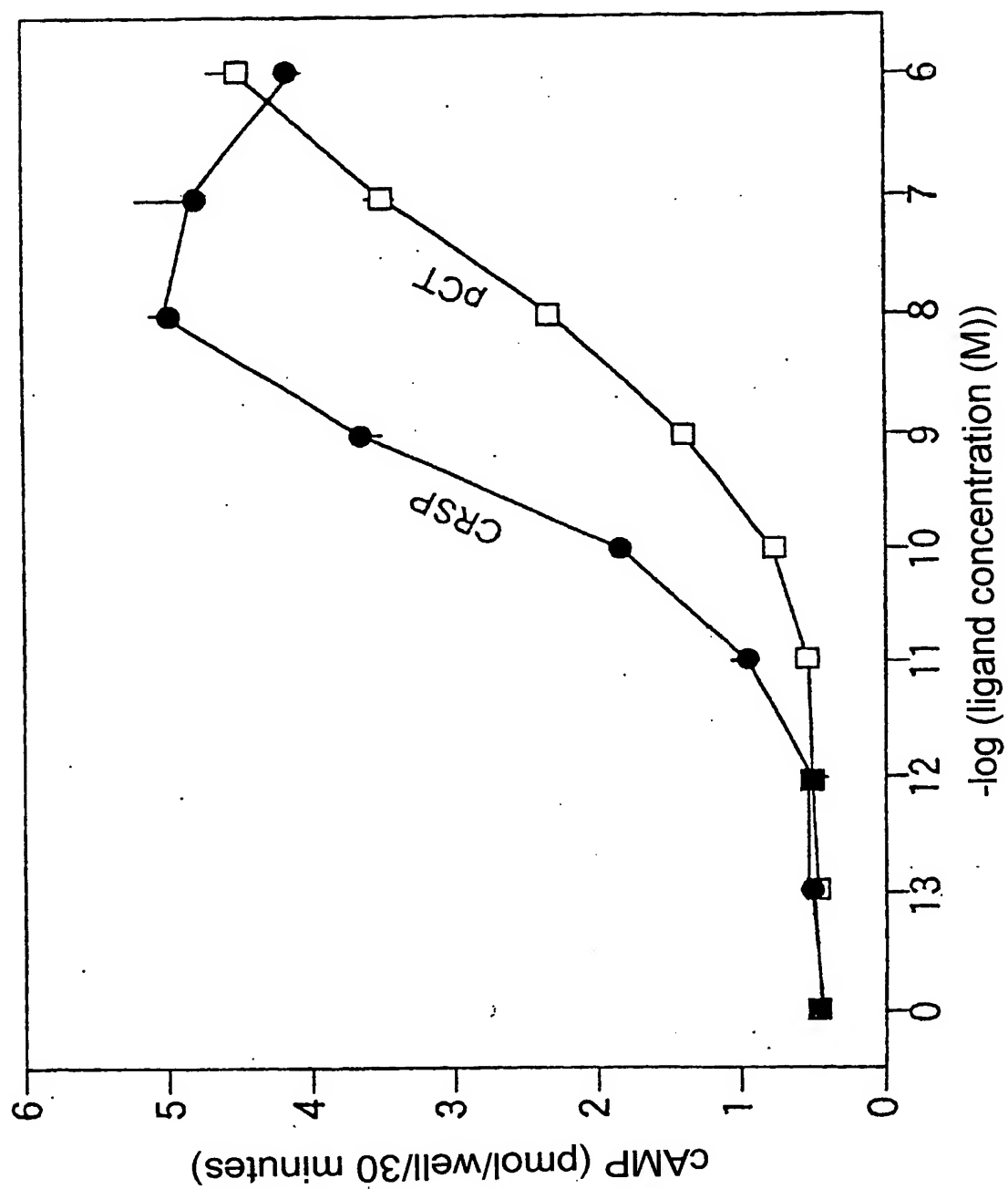


Fig. 11

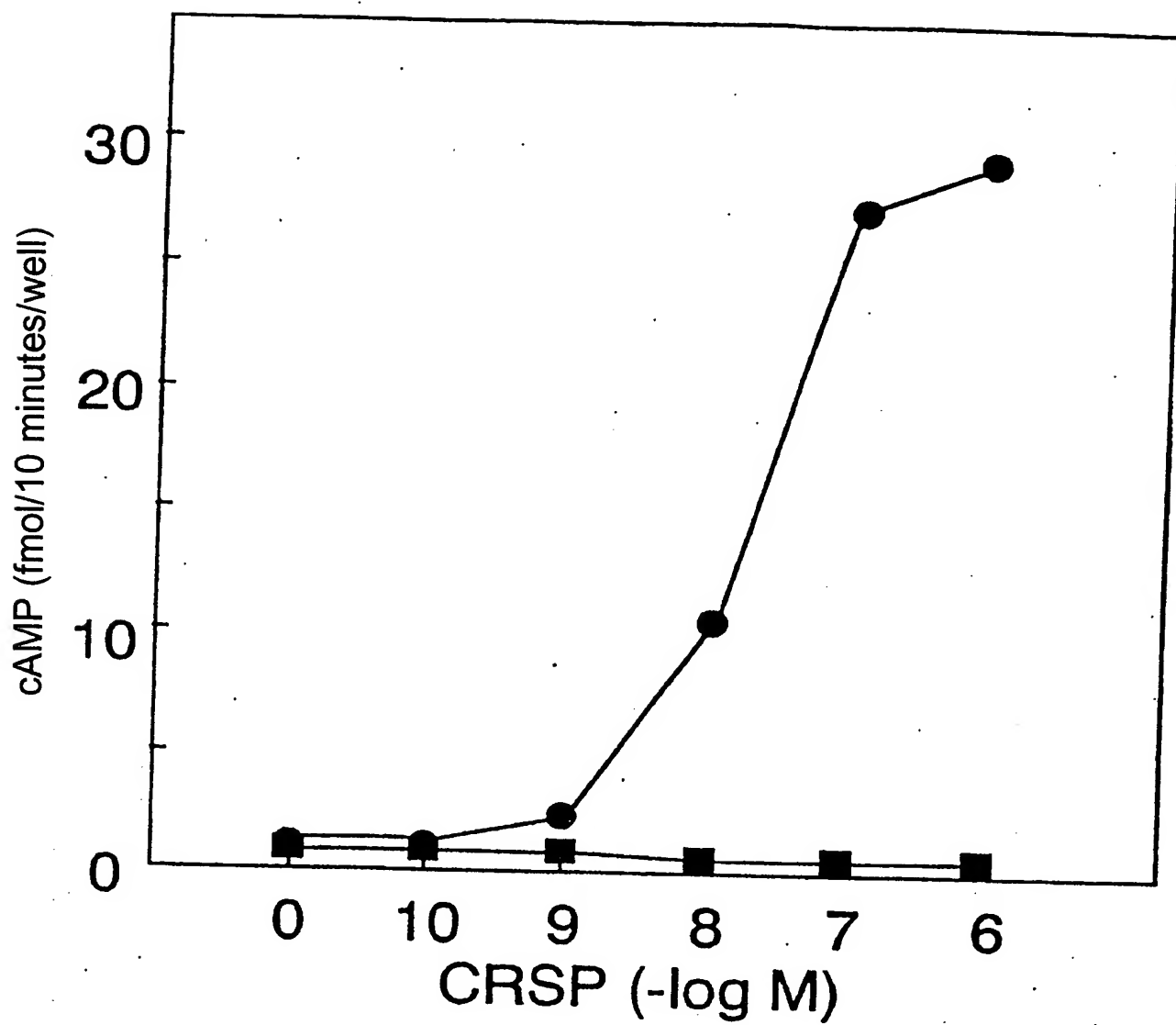


Fig. 12

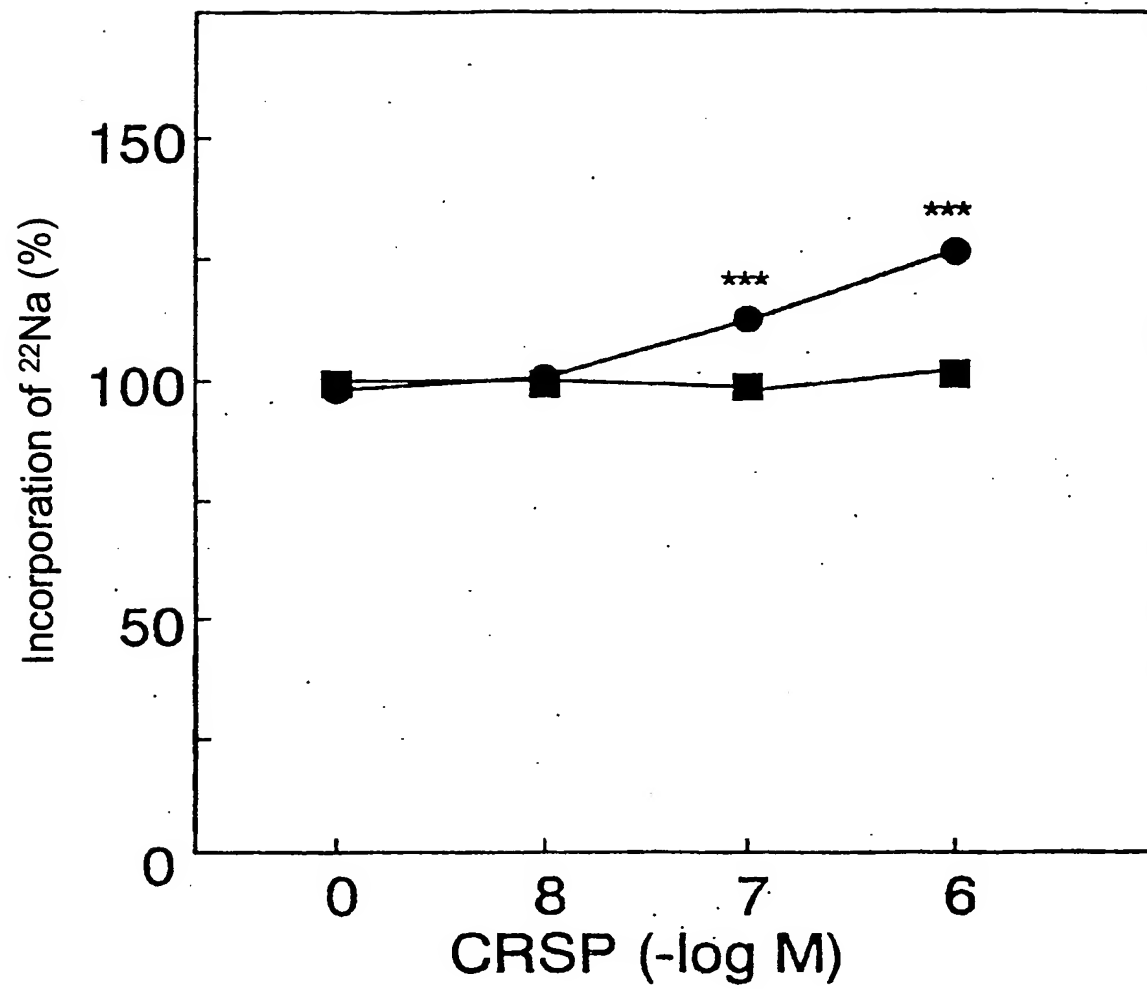


Fig. 13

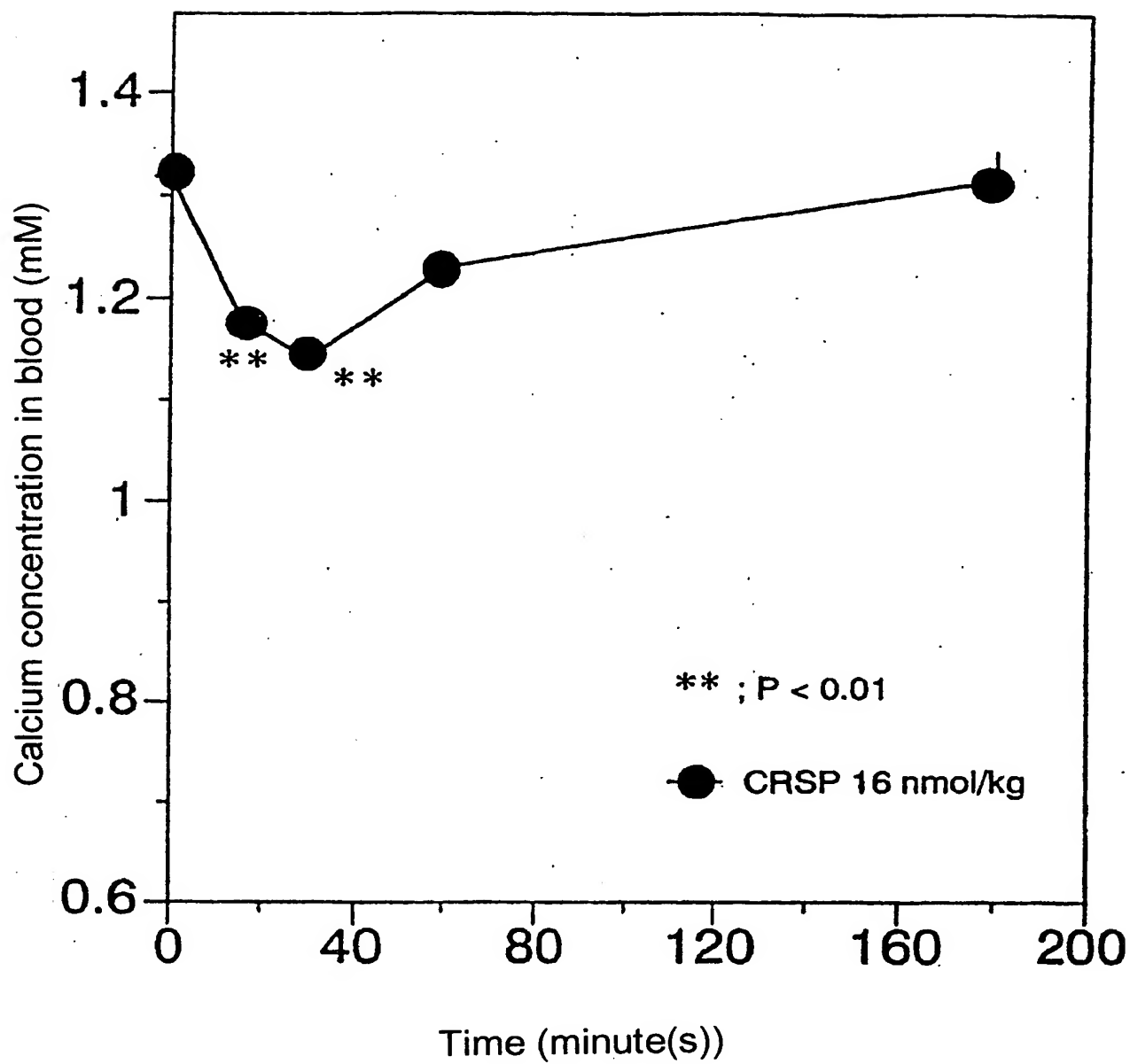


Fig. 14

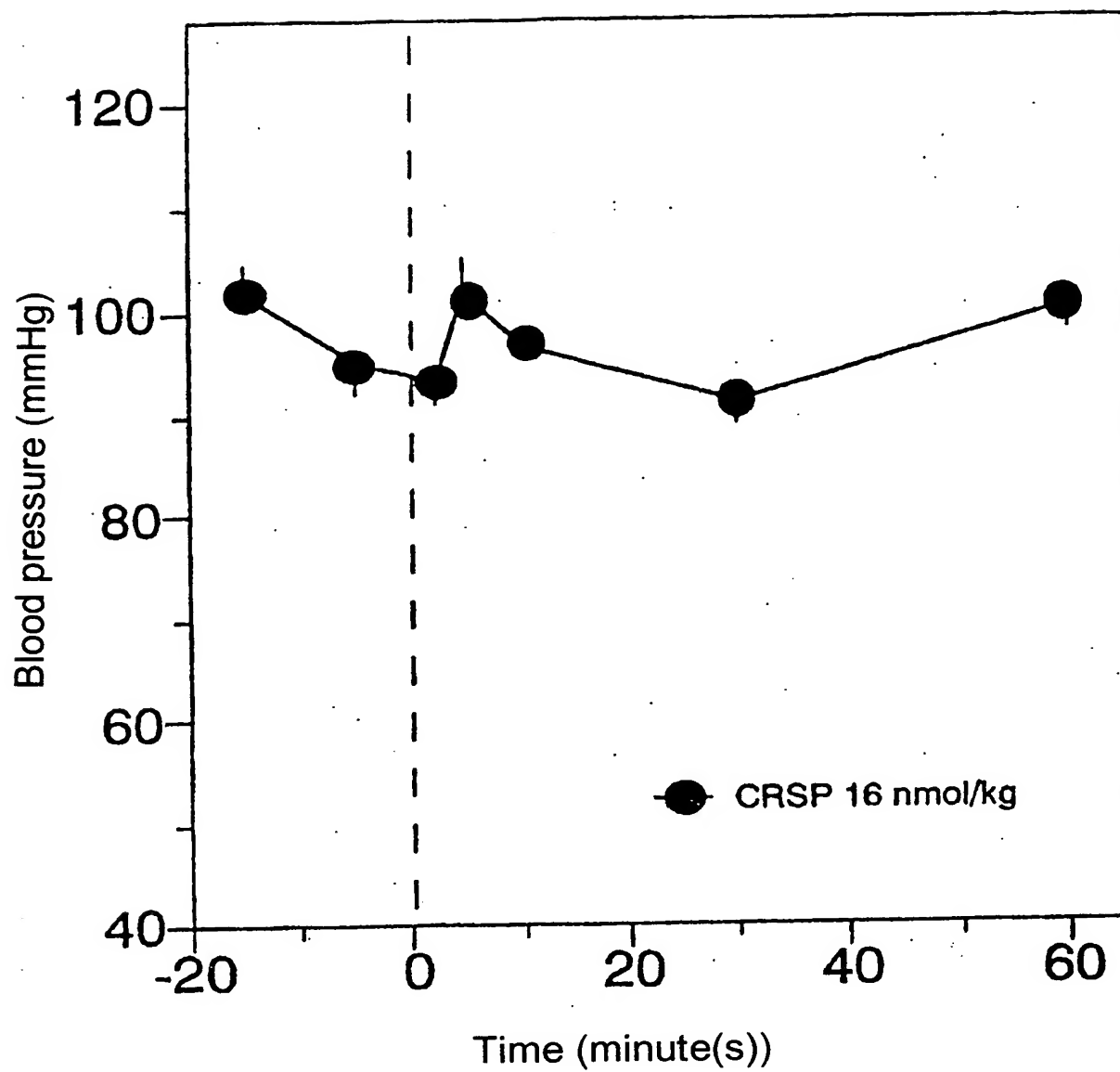


Fig. 15

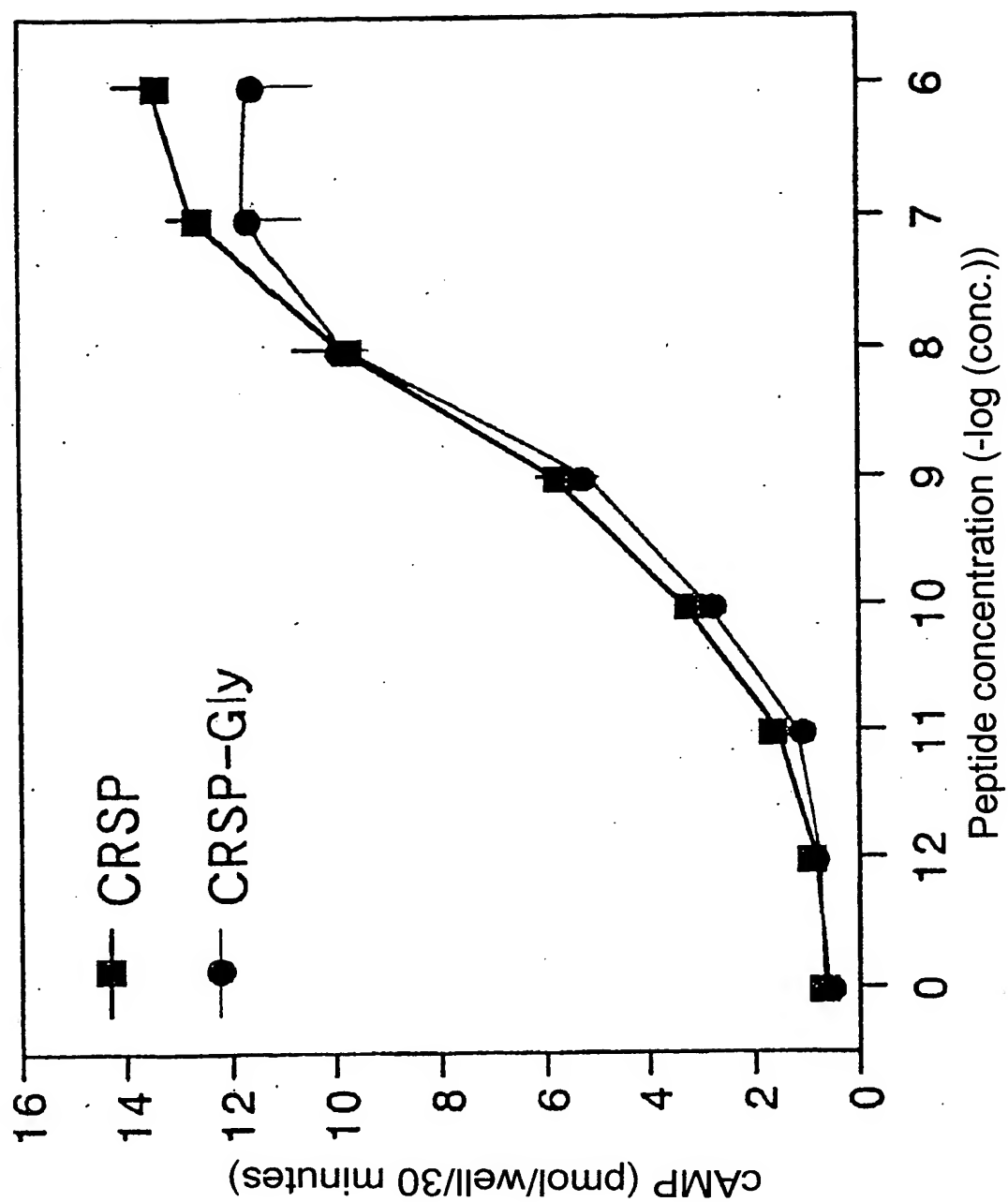


Fig. 16

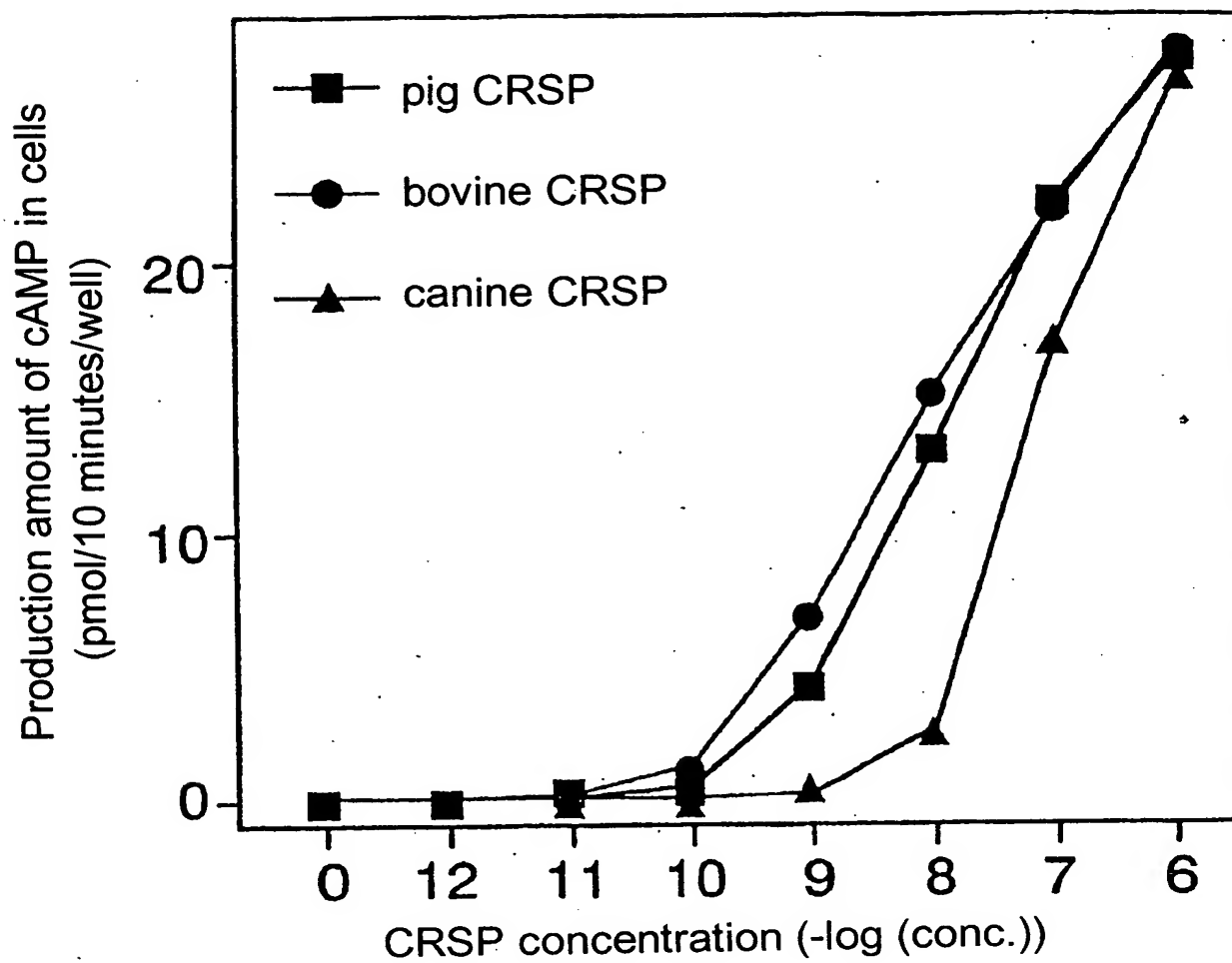


Fig. 17

CTCGAGGATCCTGCCTCTTGTTTCCCAACAATCCTGCCTTCCTGTGCTTGATTCCAGCTG 60
 CCTGAATCAGACCCCTGCTTGGGCACAGAATCATCAACCTGCTGCGCATTAACCTCCCA 120
 AACCGCACTTGGACATGGTAGTCTTAGGGGACCGGGGATGCCTTGTAATGCTGGACTCTG 180
 CTCTACAAAGATCACATAGCTGGGGATGGAGAGGGATGTGAGCCTGCGAAACCGAACAGG 240
 TAAAGTTTACCATGACGTCAAACCTGTCCTTAAATTCTGCTCACTTTGCGTGTGTTTTTC 300
 GTTGGTGCCCAACCTCCCCACCCCTCCACCCCGCCATCAATGACCTCAATGCAA 360
 ATACAAGTGGGGTGGTCCTGTTGGATGCTCCAGGTTCTGGACGCAAGTAGTGACACAATC 420
 CTGGGGCTCAGGATCTTTCCTCTCATTGGTTGCCTGGAGCTCTGGGACCACCCAGATTG 480
 AGAGCGGCGGGAATAAGAGCAGCTGCTGGTGCGGGGAAGGGTTAGAGGCACTACCCACCT 540
 CAAGTGTCTCTGCCGCTTCTTCCACAGTGCCATCGCCTGACGCCAACGCTGCTGCCTCTG 600
 CTCCCTCCTCTGCTCCAGTCCACCTGGTTCCTGCTGCCCGGTAAGCCCGGAGATTCTCTG 660
 TAAGCTGTGGTTCTGTTTCTCTCTCCCTCTCCTCCCTTCCCTCTCTCTCCATTGGATTTT 720
 CTTAGCTGATCTCTTTTCCCGTCTCAAAGTTCTCTGCTCCACTTCTCTCTGGGTCTCTTCAT 780
 CCTGTAATATGCCTTACTGCGCAATTCATTCTAGGCTCCTTTCACAGGTAACCTCTGGATG 840
 GTCTCAGTTCGGGGATTCCCTGCTCTACTCTTCTGAGCTGAGCTGGGCTCCAGTCTTGT 900
 CCCCAGCAGCAGCTGCTTAGGTCCGTGTTGGGATTTTGGAGCTCTCCAGGCACTTCAGG 960
 GAGAGGAGGATGCAGGAATAGCTTTGAGCAGAAGAACTTTCATGGATCCCATCTCCTCT 1020
 TACCTACAAGGATCGCTGGAAATGGGGTCGGGACCTGGGACAGTGCAATGGGTGGCAAA 1080
 TAGGTGCAATGACTGAGGGGAAAGTAGCTATTAACGCAAGCCCCAGTTGAAGGTTCTGG 1140
 GAACTCCCCCTCCCGCACCGCCACCCCATTTAATCTTGGGTCCCAATTTAAGGCTGTACC 1200
 AGCTTGTTTCTTACAGGGTGCTCTTTGCCAGAGTATGGAGCAGCTGGACAGTAAAATTG 1260
 GTTCTTCAGTTTCTCAGGGATTCCAACCTGCAGAGATATGTCTCCCAACTCCCCTCCCC 1320
 CCAGCCAGGTATAAGCAAAAATCAGGCATCAGGAGAGATGCTGATGGGTGCACTATGGG 1380
 AAAAGCTGTGGTGACAGGTACTGCGAGTCTGTCTCCAGGAGTCCCGGCCAACAGGTTGA 1440
 AGGTGAGAGTGTGGGTGTGCTGGGCAGGGGGCTATGGACGGAGACCTCCTCACCAGTTG 1500
 TCCTGCTAGGCTTCTTTGCTAAACCAAACATGTTGCAGGCTCACTGGATCTTCCAGCAGT 1560
 CCACTTGGCTGAGGAGGAAATGATGGTGAAAGGAAAGGACACGAGCAGCCTGAAGCCAGG 1620
 AAGCCAGGGAGTTGGAGGCAGAGGCAGGAGCAGAGCCAGGTCTGTGGGCTCAATGAACT 1680
 TGGAAGTGTACAGGTGGTGACATTGTTCTTCCCTTGCAAGGGGCACCATTGGGCTTCTG 1740
 MetGlyPheTr
 GAAATTTCCGCCCTTCCTGGTTCTCAGCATCCTGGTCCTGTACCAGGCAGGCATGTTCCA 1800
 pLysPheProProPheLeuValLeuSerIleLeuValLeuTyrGlnAlaGlyMetPheHi
 CACAGCACCAATGAGGTAAGACAGCCCTGCCAACAAGCACACTCACTTGATGAGAATGTA 1860
 sThrAlaProMetAr
 ATATAAACGTGTATATAAATTTATTATAAGGTGGCTCTGTAGAACAATGGATAGTGCCTT 1920
 GCGCTCCTATAAGTTTATCATAAGCTTTATGTGTACACAAAGTTTGTAATAGACATAAG 1980
 ATATACAGTACTCATGATTGTAAATTTTATATAACTTATCAAACCTCACAGCATGCTTTT 2040
 TTGTTTTTCATCAAATATTTGTACCTTTAGCACACGTATATGCTCATATTACCATAATTTA 2100
 AGAAATGGATTGTATCCAATTTGCCAAATACTTTGCTAGTAAATTTGTTATTAAATCTGA 2160
 TATGGGATCTACACATCTCATTTTTTACCTTCATTCAAACCTGCATTAAGCTAAAATTATT 2220
 TCCCCATTCAAACCTATCAGAAACCAGGCAACCTGGCTGTTTATCCTGGGGAGGGGCAGGC 2280
 AGGAGATCAGAACCTGTTTTTAGGCTTGCTTCCCTCCTTAGGTCTGCCTTTGGGAGCCC 2340
 gSerAlaPheGlySerPr

Fig. 17

(continued)

TTTTGATCCTGCTACCCTCTCTGAGGAGGAATCACGCCTCCTTTTGGCTGCAATGGTGAA	2400
<i>oPheAspProAlaThrLeuSerGluGluGluSerArgLeuLeuLeuAlaAlaMetValAs</i>	
TGACTATGAGCAGATGAAGGCCCGTGAGATGCAGAAGCAGAGGGCACAGGGCTCCGGGTA	2460
<i>nAspTyrGluGlnMetLysAlaArgGluMetGlnLysGlnArgAlaGlnGlySerGl</i>	
AGGTTCCCTGCCCCAAGGACAACAGGGCATCCCTTTCTTCCTCTGGTCAGGCCCAGGAAGG	2520
CATATTTTAAAGTCACTTTTGAGTTTTCTGACCCCCCTGGACATGTCTGTGGGATGATTA	2580
TGGCATTTCCTGACGGCCTAGGATTTTCTGCTGTGATGACCTTTTCTAGCAGAAATAC	2640
TCAAGGTTCACTGGTCCTCTCAAGGCAGTAGTCTTCCATGACGATTCTGTTCGTACAGCAC	2700
CTGCACTCAACCTCTCACTGACGGGCCTTTTCTTTCTTTATCCACAAATCAGCATCAGT	2760
<i>yIleSer</i>	
GTCCAGAAGAGATCCTGCAACACTGCCACCTGCATGACCCATCGGCTGGTGGGCTTGCTC	2820
<i>ValGlnLysArgSerCysAsnThrAlaThrCysMetThrHisArgLeuValGlyLeuLeu</i>	
AGCAGATCTGGGAGCATGGTGAGGAGCAACCTGTTGCCACCAAGATGGGCTTCAAAGTC	2880
<i>SerArgSerGlySerMetValArgSerAsnLeuLeuProThrLysMetGlyPheLysVal</i>	
TTTGGTGGGCGCCGCAGGAACCTTTTGGATCTGAGCAGTGGGATGATTCCAGGAGGAAGGT	2940
<i>PheGlyGlyArgArgArgAsnPheTrpIle***</i>	
GACTGCCCTTTTTGTACCTTCGGGTGGGAGGACAGAGGACTGGGTATTGCAGGGGTGCAT	3000
TCCACACCCTAACCCCTCTGTGAGCGCATGGGGGTAAAACCTCCACATGGCAAGGTGCCCA	3060
CACCAGTGTCTGGAGAAAGGACTGATAATCCCTATAACTGAAACATTGGGCTCTTTCTCT	3120
CTGTTTCTCCAGTCTCTCCCTGTGACACTGACATCATCTGCCAGGAAATATAGACCCTGT	3180
TTACTTAAAACACTGTTCCCTGGGTATTAATTGGGGTCCAGCTCTAGCATTAGAATTTGA	3240
AAGGTAATGACCCTACCCCTTTTGGAGCATACCTTACAATGTTATGAACTTGGAGCATAGA	3300
CTCGGATTCAAATACTGTGTCTGTCTTCCACTAACTGTGACCATAGGCAAGTATGCCTCT	3360
GAGCCTCAGCTTCTCCTTGTAACCTGAAGGCAACAATAGTATCCTCAATATAAAAATTAA	3420
TTAGTATAACATATGACAAGAGCCTGTTAACTAAGAATTAATAACATCTGTACTTTTT	3480
TCCCTCCTAGGTTACTATGACTCTGAACTCTACTTCGTTTAATTTACAATGAAAGCAACC	3540
TACTAAAAAATAGCATGGAAGACATCCATGTATGCATGCTTCTGGAAACTGAAAACACTC	3600
TTTTCTTTGAAATAAACTAAACTAAATGCAAAATAAAATCAATGCATCAATGCAGTTAC	3660
CTTGTGTGCATCTTTTGTGTATATGATTCTATAATATGATGCATGTCTCATTAGGTTTAA	3720
TGGTAGCAAATCTGGCCCCTGTCAGCCAACCTGTTGGTGGGGGCAGCTCTGCTAAACCTC	3780
AGGGTCACATGAATTC	3796

Fig. 18

GGATCCACTAGTTCTAGATAAAATGGACAAATACCTAGAAACAGAAGACCTACCAAGATG	60
GAAGGATGAAGAAATAGAAAATTCAAATACACCTATGACTAGGAAGGAGAATGAAGCATT	120
AATCCAAAATCTTCCAACAAAGAAAAGCCCTGGATACGATGGCCTCATTGGTGAATAGTA	180
CCAGACATTTAAAGAAAACGAATACCAATCCTTGTCAAACCTTTCCAAAACCTGAAGAG	240
AAAGGACACACCCTAACCTATTCTATGAGGCAGGCCAACATTACTCTGATACCAAAGATG	300
GAGAAAGATTCTGCAAGGAGAAAACCCCTACAGACAAAATCCTTTATGACATGGATGTGG	360
AAACCCCTCAACAGTATGCTAGGGAATTGAATTCAGAAGCGTATTAAAAGGATCCTACAAC	420
ATGACCAAGTGGGATGAATTTCTGGAATGCAAGGATGATTCAAATATGAAAATTGATCA	480
AAGTGTATATCACAATAATGGAATGTAGGGAAAAACACACCTGATTATTTCCACTGATA	540
CAGAAAATTATTTAGTAAATTTCAATACCTTTTCAGGATTAAAAACAAAACCTAGGTATA	600
GAAGGAGACTGCCTCAGCACAATACAACTATATATGAAAAACCAACACCAACACCATAAT	660
CCAGGGTGGAAAACCTGAAAGCTTTTCCCCTAAGATCTGGAAGAAAATGGAAAAAAATTTT	720
TAAGAATTTTCAGACAGATTTGGGTCTCTGGTACACTCTGAGAAATCATCTTTTAGAATT	780
TTTTTTTTTTTAAAAATAAGCACAGAATTTTCATTTAAAAGAAGGGAAATAACATAGCCTT	840
CAGAGTTTATCAGGAGGTGTAATTTTTTTTTTCCACACTAGATTGTGGCTACCTGATGCTA	900
ATTTTGAGGTTTAAACATAATGAAATAAGATTGTACAGCCAAGTGCCAGCTAGTCATGGA	960
ACTTTTACCTCAGTACTGTTTAGTGCTTCAGTCCTAAGAAGTTTCAGGGAGGGCTGCGTG	1020
CAATACAAGTAATCGGTACTTGCTGAAGGTCTAAAATTTTCGAGTGCACTTGGTAAATCAG	1080
GGATGGGCGCAGAGGAGACTGGTTCTGTAAGTCTAGACTAGTGAACCTAGAAATTTAGAAA	1140
GGGTACTTTTGTGCTCCAAGCAAATCCTGTTCTACCTAACTAGGTCCAAATGCTCTGCAG	1200
GCTGTAGTTAGAGCCCTCTCATAGCAGGGAGACTGCCTTGGTGAATCTGCCAGAGGAAAT	1260
GAATTTCCATTACATTCATTCAACAAACATTGGGCGAGTGCCACCTCATGTGCAAAACA	1320
TGGTGCTAAGTGCTAAAGAAAAGATGTTGTTTTGTAAACTTACCCGCAGCTCAGAGCCAG	1380
GACTTCTTGGAAGTCAAGGACTTGAGGAAGGAGTTCATCTCAGCCCCTCCCTCACTGG	1440
AGAGACTGGCTTTTCTTTCCAAGTAAAGCTTAAACTGCTGGAGGCTAAGTTAGCACCTT	1500
CTGGGGGCAGACCCTGATTCCTGCCTCTCATCCCCAGCCCTTTGTGTGTGGGCGCCAAAG	1560
ATTTCTGAGTGAGGAATGAATGTTGGCTTTGAACAGGAAAGGCACAAGTGGCAGCCAAGG	1620
GTAGAATGCTGAGCCTACAAATTAACATAGTTACAAATTTGTCTTCTAAAGGAGTCGTTT	1680
CTTAGCCATAGTGCAGCCACCTTTGCATTGATCAAACTGTGGTTCTTCCAATGAAAAAA	1740
GACATCCCCAGACACATACTTACAAATGATTTTCAGAAGATTGATAGGTCGGAAATCTC	1800
AGGTTTTTGATTTTATTTGCAAAAGCGTTTTGCGCCTGAGTTTTAACTTTTTTTTTTTT	1860
TTTTTTTTTTTTGTATTTTTTCACTTCTAGGGCGGCTTCGGCGGCATATGGAAATTCCAG	1920

Fig. 18

(continued)

GCTAGGGGTCTAATAGGCGCCATAGCCACCGGCCTACGCCAGAGCTACTGCAACGCTGGA	1980
TCCGAGCCGCATCTGCAACCTACACCACAACCTCACGGCAATGCCGGATCGTTAACCCACT	2040
GAGCAAGGCCAGGGATCGAACCCGCAACCTCATGGTTCTTACTCAGATTTCGTTAACCACT	2100
GCGCCACGACGGCCACTCCAACCTACCAGACTCTTAATTAAGTAGCAGAGTCCAATTTAC	2160
ATGCCGCACCACATCTGTTACCCCGAGTTAGCGAAGTTGGTCTTGGAACCTAATCCTCAC	2220
GGAAAGCCAAGCCGAGTACTCATAATTATAGTGCTGAACCCCCAAACCCTGGTCTGGCCT	2280
GTGCACCCAATTTTGTGCTGTAGTAGAAACCAGGATTTACGGAGCCCCGAGCAGTCCGCCA	2340
TCCTGAACTCTTCTCTTTCTCACCTTGCCTTCATCCTGGAGTGCACCTGCCCTCTATGAA	2400
CCAGTTTTTCCGTTCCCTTGGTCTCCCGATCCGTTGTCTATCCTGAGGAGAGCGAGATGC	2460
AAGCACCCGATTCCCTAGCCCCAATATTTTATTCTCTTGCGAAGGAGAAAAGTTGAATAA	2520
GGGTATCTTGTAATGAGATGTTCCGAGTCCAGAGAGCACAAACCGGCAAGGGGAACAGA	2580
TGTGCCGCGAGGCAGGTGTGCGGAAAGATATAGAGAAGGCTCAGGTTCCGGACCTGTGGCT	2640
CAGGTCACACTCATGGCAGAGTTCGGTTTAATTTCCGGCTCTGCCCTGGGGGAACCACTTAA	2700
CTGGGGTCCCTTGCTGCCCTCCACCGGCCCCCGATGCTGTTGCAGCGTTTGCCGCGCTGGA	2760
GGGTCTGTACAGGCTGCTGCGGTTTATCGCTGTGTGCTCAGACACGGTGATCCTGAGCAG	2820
CATCCGAAC TGATTGGGGTAGATGTGGGCACAGGGCTGGAATCACAGGTCACCTGGAACA	2880
TCTTGGAACACAGCAGCCGGAAGCAAGGGGCAGCTGGGCAAATGGTTCTGGGACATTGAT	2940
GGGCTTAGATGATGAATGGTGGGGCTGGAGGTCGGCTTGCGCGCTTGGAAGCATCTATG	3000
CCGTGCACGTCCCTGCCCAAGCCCAGTAGGGCACCATCTTTCCCATATGGTGGACCGAC	3060
CACCCAGCGCGACTCCAGACATCCGCACAGAGGTGGGGATTGGGCAAATGGATCGCGATC	3120
GCACAGAATCCCCCTGTGCACTTCCCTGGTAAGCTCTTCTCGATCCCTCCCTGGGTGGAGA	3180
GCAGGTACATGGCTACTAATGATACCACTCCTTGAAGACGGGAATATGATGCCCCGTTC	3240
AAAAATTAATATATTGAGGTGCTAGAAGACACTAGCCCGATGATCTTACTACCTAGAAAA	3300
GGCACAGCTGGAACAAAGTTTCCGTGTGACAAAGACTGTGATCCTGCCTCTTGTTTCCCA	3360
CAAATCCTGCCTTCCCTGTGCTTGATTCCAGCTGCCTGAATCAGACCCCCCTGCTTGGGCAC	3420
AGAATCATCAACCTGCTGCGCATTAACCTCCCAAACCGCACTTGGACATGGTAGTCTTAG	3480
GGGACCGGGGATGCCTTGTAACGCTGGACTCTGCTCTACAAAGATCACATAGCTGGGGAT	3540
GGAGAGGGATGTGAGCCTGCGAAACCGAACAGGTAAAGTTTACCATGACGTCAAACGTGTC	3600
CTTAAATTCCTGCTCACTTTGCGTGTGTTTTTCGTTGGTGCCACCAACCTCCCCACCCC	3660
CTCCCACCCCCGCCATCAATGACCTCAATGCAAATACAAGTGGGGTGGTCCTGTTGGATG	3720
CTCCAGGTCTTGACGCAAGTAGTGACACAATCCTGGGGCTCAGGATCTTTCCTCTCATT	3780
GGTTGCCTGGAGCTCTGGGACCACCCCAGATTCAGAGCGGCGGGAATAAGAGCAGCTGCT	3840

Fig. 19

GGTGCGGGGAAGGGTTAGAGGCACTACCCACCTCAAGTGTCTCTGCCGCTTCTTCCACAG 3900
 TGCCATCGCCTGACGCCAACGCTGCTGCCCTCTGCTCCCTCCTCTGCTCCAGTCCACCTGG 3960
 TTCCTGCTGCCCCGTAAGCCCGGAGATTCCCTGCTAAGCTGTGGTTCTGTTTCTCTCTCCC 4020
 TCTCCTCCCTTCCCTCTCTCTCCATTGGATTTTCTTAGCTGATCTCTTTTCCCGTCTCAA 4080
 AGTTCCTGTCCACTTCTCTCTGGGTCTCTTCATCCTGTAATATGCCTTACTGCGCAATTC 4140
 ATTCTAGGCTCCTTTTACAGGTAACCTCTGGATGGTCTCAGTTCGGGGATTCCCTGCTCTA 4200
 CTCTTCCTGAGCTGAGCTGGGCTCCAGTCTTGTCCCCGCAGCAGACGTGCTTAGGTCCGT 4260
 GTTGGGATTTTGGAGCTCTCCAGGCACTTCAGGGAGAGGAGGATGCAGGAATAGCTTTGA 4320
 GCAGAAGAACTTTTCATGGATCCCATCTCCTCTTACCTACAAGGATCGCTGGAAATGGGG 4380
 TCGGGACCTGGGACAGTGCAAATGGGTGGCAAATAGGTGCAATGACTGAGGGGAAAGTAG 4440
 CTATTAAACGCAAGCCCCAGTTGAAGGTTCTGGGAACTCCCCCTCCCGCACC GCCACCCC 4500
 ATTTAATCTTGGGTCCCAATTTAAGGCTGTACCGGCTTGTTCCTTACAGGGTGCTCTTTG 4560
 CCAGAGTATGGAGCAGCTGGACAGTAAAAATTTGGTTCTTCAGTTTCTCAGGGATTCCAAC 4620
 TGCAGAGATATGTCTCCCACTCCCCCTTCCCCCAGCCAGGTATAAGCAAAAATCAGGC 4680
 ATCAGGAGAGATGCTGATGGGTGCACTATGGGAAAAGCTGTGGTGACAGGTACTGTGAG 4740
 TCTGTCTCCAGGAGTCCCGGCCAACAGGTTGAAGGTGAGAGTGTGGGTGTGCTGGGCAG 4800
 GGGGCTATGGACGGAGACCTTCTCACCAGTTGTCTGCTAGGCTTCTTTGCTAAACCAA 4860
 GCATGTTGCAGGCTCACTGGATCTTCCAGCAGTCCACTTGGCTGAGGAGGAAATGATGGT 4920
 GAAAGGAAAGGACACGAGCAGCCTGAAGCCAGGAAGCCAGGGAGTTGGAGGCAGAGGCAG 4980
 GAGCAGAGCCCAGGTCTGTGGGCTCAATGAACCTGGAACCTGCTACAGGTGGTGACATTGT 5040
 TCTTCCCTTGCAGAGGGGCACCATGGGCTTCTGGAAATTTCCGCCCTTCCTGGTTCTCAG 5100

MetGlyPheTrpLysPheProProPheLeuValLeuSe

CATCCTGGTCTGTACCAGGCAGGCATGTTCCACACAGCACCCGTGAGGTAAGACAGCAC 5160
rIleLeuValLeuTyrGlnAlaGlyMetPheHisThrAlaProValAr

TGGTGGCAGTGCTCTCGCTTCCCACGGCCCCCGGAATCATATAGTTCTGTATTGTGAGTT 5220
 GTGCTGTGGTGAGTCTGGCTCTTGGTGGGCTTCTGTGTATAGGGGTGTGGGGTCTAAT 5280
 GTATGAATATAGTCATGTATATAAGTTTATTATAAATATTTTGTGATCCAAGATAATATC 5340
 ACAAAGTTTACAAATAAATAGAAGATATACAGTATTCATAAATTTCTAAACTCACTG 5400
 AACCTTACAGCATGTTTTTGTGCTTTTTATGAAATGTTTATAACTTTAGCAAACCTATA 5460
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 ATTTGTTATTAAATCTGAAAGGTAATCTATACAATTTCTCACCCCTCTTTCAAATTTATAT 5580
 AATATGAAACCATTTTTCATATTCAAACATCATTTAATTTTAAATAATGGCTGTATTAA 5640
 CACTAAGCTCATACAATTCCTGAAGATCTAACCATCAGCTTTCAAAGCCTACATGATGC 5700
 ACTTTCAGCAGAACTACTTTGTGGACACCCAGAGCCTAACTCATGGTGAAGCAGCATTT 5760
 TTGGATGAACACTAGCCTTATGTCTGACCGTTGAGAATTTTCATCAGCCTTATTTCTCAGA 5820
 GGAAGTGGCAGAAACCAGGAAATCTGGCTGCTTATCCTAGGGCTGTGGTAGGCTCAGAGC 5880
 GCATGTTGGGCTTGCTTTCCCTTCCAGATTGCCCTTGGAGAGCAGCTTTGATTCTGCCA 5940

gLeuProLeuGluSerSerPheAspSerAlaT

CTCTCACAGAGGAGGAAGTGTCCCTTCTACTGGTTGCAATGGTGAAGGATTATGTGCAGA 6000
hrLeuThrGluGluGluValSerLeuLeuLeuValAlaMetValLysAspTyrValGlnM

Fig. 19

(continued)

TGAAGGCCACTGTGCTGGAGCAGGAGTCAGAGGACTTCAGGTCAGTCTTTGCACCCCTCC 6060
etLysAlaThrValLeuGluGlnGluSerGluAspPheSe

CAGAATATGGCTTACCCTCTCCCTAGAGTACCAGGAAGGCATATCCTTAAGAATGAGATT 6120
TGTTATAGTGCCATAAGCCTTGATGTCCAGTCTCATAAGCCTTGGTTTATTTTTAGTTTA 6180
TTACACAGGAGAGATTGTCTATTACAGTTCTGATTTCCAGGTCCAGTAATGCAGAGCCAC 6240
CTTTGGGTTTTCTGACACCCCTGAAAATGTCTATGGGGAGTGATGATGCATTTTCCCAA 6300
AGCCCTATGTTTTCTGTTGGGATTTTGTGTTTAGCAGAAACATTTTCAGGTTCACTGGTC 6360
CCTCTCAGAGCTGTAATTTTCCACTGATGGTCAGTCTGGGGGAATCACTTGCCCTCAA 6420
GCTGTCATTGGCAGGCCTTCTCTTGTCTCCATCCTGAAAATCAGCATCACTGCCCAGGA 6480
rIleThrAlaGlnGI

GAAATCCTGCAACACTGCTAGCTGTGTGACCCACAAGATGACAGGCTGGCTGAGCAGATC 6540
uLysSerCysAsnThrAlaSerCysValThrHisLysMetThrGlyTrpLeuSerArgSe

TGGGAGCGTGGCTAAGAACAACCTTCATGCCACCAATGTGGACTCCAAAATCTTGGGCTG 6600
rGlySerValAlaLysAsnAsnPheMetProThrAsnValAspSerLysIleLeuGly**

ACGCCGCAGAGAGCCTCAGGCCTGAGCTGTGAAATGACTCCACAAAGAAGGTGACTGCTC 6660
*

TAGAACATGGGATAGCAGGGCAAATGGCTGGGTATTTTCAGGGGTGTTGGCTACACTCTAA 6720
CCCTCCCTGAGCCTGTACTGTAAAAAAAATCCATAATGAAGTTGCTGACCCCATTTATCC 6780
TCAGAAAGAAAAGAGAATCCTAATAGCCAAAACCCCTATAACTTAGGTTTCAATTTCTATT 6840
TTTTCCAGTGTCTCCAGTGACTCTGAGGTCATCTGTCAGGAAACATAGATTCTATTCTT 6900
TTTTCTTTTCTTTTGGCTACACCCAAGGCATGTGAAAGTTTTTGGGCCAGGGATTGAAT 6960
CTGAACCATAGCTGTGACCTATGCAGTACCTGTGGCAACACTGGATCCTTAACCCAATGT 7020
ACCACATCAGGAACCTCCTAGGTCCTATTATTTAAAACACTGTTCCCTGCAGTTATAATTG 7080
TGATTATTCTAGTTTTTGAGTTTGAAAGGTAATGATCTTATCCAGTGAGTTTGAAGTATA 7140
ACTACAATGTCACATATATCTGAATTCAGAGCATTGACTTGGTTTCAAATGCGATGCTG 7200
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CATGGTAAGAGCCTCACTATTAATAAGTAATAATATCTAGCTCTTATTTTTTTTTTCTCC 7380
TAGGTCACCAAGGAACCTGAACCTATTTCTTTTAATCTGCAATGAAAGCAATTTATTTGA 7440
AAAATAGCATGGAAAACACACATATATGCATGCTTCTTGCTTGAAATACAGCTTTTAGCT 7500
TGAAATAAACTAAAACTAAATGCAGAATAAAATCATTGCAGCTACCTGATATGTATCATT 7560
TTAATATTTGATTCTGTATTCTATAAGTATGACTCATGTCTCGCTGGCTTATCTGGTAGC 7620
AAATCTGGACCCTGTCAGCCAACCTGTTGGTGGTGGCAGCTCTGCTAAACCTC 7673

Fig. 20

CTCAAGTGTCTCTGCCGCTTCTTCCACAGTGCCATCGCCTGACGCCAACGCTGCTGCCTC	-52
TGCTCCCTCCTCTGCTCCAGTCCACCTGGTTCCTGCTGCCCCGAGGGGCACCATGGGCTTC	9
M G F	3
TGGAAATTTCGCCCCCTTCCTGGTTCTCAGCATCCTGGTCCCTGTACCAGGCAGGCATGTTC	69
W K F P P F L V L S I L V L Y Q A G M F	23
CACACAGCACCCGTGAGATTGCCTTTGGAGAGCAGCTTTGATTCTGCCACTCTCACAGAG	129
H T A P V R L P L E S S F D S A T L T E	43
GAGGAAGTGTCCCTTCTACTGGTTGCAATGGTGAAGGATTATGTGCAGATGAAGGCCACT	189
E E V S L L L V A M V K D Y V Q M K A T	63
GTGCTGGAGCAGGAGTCAGAGGACTTCAGCATCACTGCCCAGGAGAAATCCTGCAACACT	249
V L E Q E S E D F S I T A Q E K <u>S C N T</u>	83
GCTAGCTGTGTGACCCACAAGATGACAGGCTGGCTGAGCAGATCTGGGAGCGTGGCTAAG	309
<u>A S C V T H K M T G W L S R S G S V A K</u>	103
AACAACCTTCATGCCCCACCAATGTGGACTCCAAAATCTTGGGCTGACGCCGCAGAGAGCCT	369
<u>N N F M P T N V D S K I L</u> G	117
CAGGCCTGAGCTGTGAAATGACTCCACAAAGAAGGTCACCAAGGAACTGAACTCTATTTTC	429
TTTTAATCTGCAATGAAAGCAATTTATTTGAAAAATAGCATGGAAAACACACATATATGC	489
ATGCTTCTTGCTTGAAATACAGCTTTTAGCTTGAAATAAACTAAACTAAATGCAGAATA	549
AAATCATTCAGCTACCTGAAAAAAAAAAAA	579

Fig. 21


GCCCAGCTTACGTCTCCTTTCTCCGCCAGTGCCATCACCTGCCACCAGCGCGGTTGTTGC	-52
TTCTCCCACCTTGGGCTCCAAGCTACCTGGTTCCTGCATCCAGAGGGGCACCATGGGCTTC	9
	M G F 3
TGGAAGTTCCCCCCTTCTGATCCTCAGCATCCTGGTCCTGTACCAAGCAGGAATGCTC	69
W K F P P F L I L S I L V L Y Q A G M L	23
CATGCCGCGCCATTTCAGGATGGCTTTGGGAAGCAGCTTTGATTCTGCCACACTCACGGAA	129
H A A P F R M A L G S S F D S A T L T E	43
GAGGAAATGTCCCTCCTACTGGTTGCAATGGTGAAGGATTATGTGCAGATGAAGGCCACT	189
E E M S L L L V A M V K D Y V Q M K A T	63
GTGCTGGAGCAGGAGACAGAGGACTTCAGCATCACCACCCAGGAGAGATCCTGCAACACT	249
V L E Q E T E D F S I T T Q E R <u>S C N T</u>	83
GCCATCTGTGTGACCCACAAGATGGCAGGCTGGCTGAGCAGATCTGGGAGCGTGGTTAAG	309
<u>A I C V T H K M A G W L S R S G S V V K</u>	103
AACAACCTTCATGCCCATCAACATGGGCTCCAAAGTCTTGGGCGCGCCGCGCAGACAGCCT	369
<u>N N F M P I N M G S K V L</u>  R R R R Q P	123
CAGGCCTGAGCTGTGAAATGACTCTAAAAAGAAGTTGAACTCAAGTTGCTTTCACTGCAA	429
Q A *	125
AGTTGCTTTCCCTGCAAATTAAAAGAACCAATTTGAAAAATAGCATGGAAGACACACATA	489
TATGCATGCTTCTTGCTTGAAATACAACCTTTTGCTTGAAACAACTAAACCTAAATGCA	549
GAATAAAATCATTGCAGTTACCTGA	574

Fig. 22

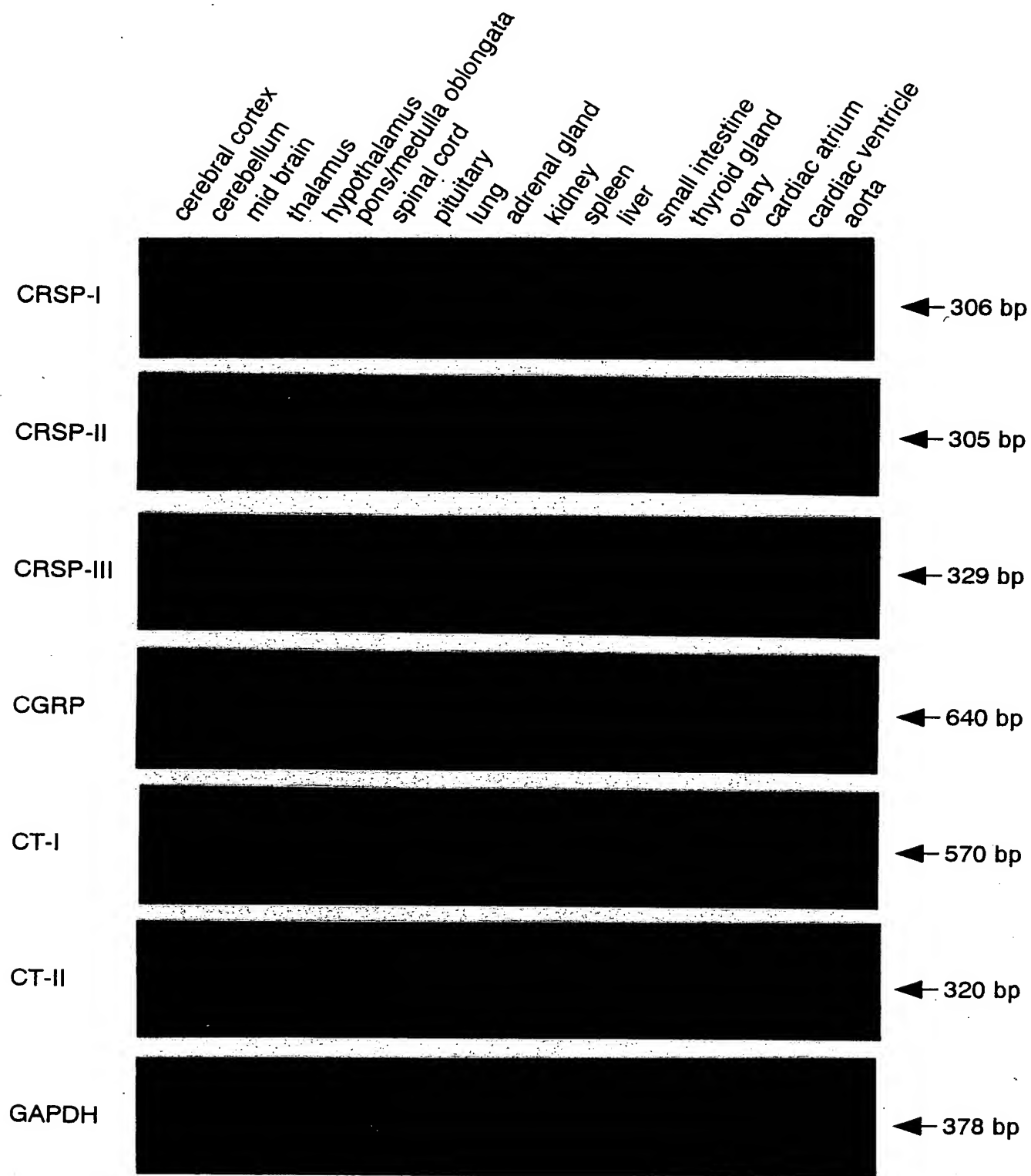
GCCCAGCTTACGTCTCCTTTCTCCGCCAGTGCCATCACCTGCCACCAGCGCGGTTGTTGC	-52
TTCTCCCCTTGGGCTCCAAGCTACCTGGTTCTGTCATCCAGAGGGGCACCATGGGCTTC	9
M G F	3
TGGAAGTTCCCCCCTTCCTGATCCTCAGCATCCTGGTCCTGTACCAAGCAGGAATGCTC	69
W K F P P F L I L S I L V L Y Q A G M L	23
CATGCCGCGCCATTCAAGATGGCTTTGGGAAGCAGCTTTGATTCTGCCACACTCACGGAA	129
H A A P F R M A L G S S F D S A T L T E	43
GAGGAAATGTCCCTCCTACTGGTTGCAATGGTGAAGGATTATGTGCAGATGAAGGCCACT	189
E E M S L L L V A M V K D Y V Q M K A T	63
GTGCTGGAGCAGGAGACAGAGGACTTCAGCCTGGACAGCTCCAGAGCTAAGCAGTGCAAT	249
V L E Q E T E D F S L D S S R A K <u>Q C N</u>	83
AATCTGAGTACCTGTGTGCTGGGAACATATACATGGGACGTCAACAAGTTTTATGCATTC	309
N L S T C V L G T Y T W D V N K F Y A F	103
CCCTTAACTACAACCTGGGATTAGAGTATCTGGCAAGAAATGGGTCAGGGCCAGAGTCTCA	369
P L T T T G I R V S <u>K</u> K K W V R A R V S	123
GAGAAAGTCCATTATCCCTCAAGGCAGCATACCCTAAGGTGCTTAAGAAGGCCCCCACC	429
E K V H Y P S R Q H T L R C L R R P P P	143
CTCCTCCTTTCTAGTTCTCTCCTAGAATTTGCATGTGTTCTTCTCTGGTTGCTCTCTGA	489
L L L S S S S P R I C M C S S L V A L	162
GCTGCTATCAGCAGCTTTCCTTGTGGCCATGGATGTCTGGAATATCAGAGAGGAGGTGGG	549
GGGTGGGGGCAGGCAGGCCAGAAGAAAATCACTCAGGAATAGATTAGGAGAGAATGGGCA	609
GCCCTGTGAGTGCCTGTGGATTTACAGCAGAGCTTCTCAGTCCTGCTTCTGAACATGCT	669
TTTCACTAGGGAATAAAAGTAT	691

Fig. 23

SCNTASCVTHKMTGWLSRSGSVAKNNFMP-TNVD**SKIL**-NH₂ pCRSP-2
 SCNTAICVTHKMA**GWLSRSGSVVKN**NFMP-INMG**SKVL**-NH₂ pCRSP-3
 SCNTATCMTHRLVGLLSRSGSMVRSNLLP-TKM**GFKVFG**-NH₂ pCRSP
 SCNTATCVTHRLAGLLSRSGMVKS**NFVP**-TDVGSEAF-NH₂ pCGRP
 YRQSMN**NFQGLR**SFGCRFGTCTVQ**KL**AHQIYQFTDKDKDGVAPRSKIS**PQGY**-NH₂ pAM

CSNLSTC**VL**SA**YWR**NI**NN**EH**RF**SGMG**FG**PE**TP**-NH₂ pCT
 pECNNLSTC**VL**GT**YTWD**VN**KFYA**EP**LT**TT**GI**RS-NH₂ pCT-2

Fig. 24



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